

```
!!SEQUENCE_LIST 1.0
! FINDPATTERNS on GenBank: * allowing 0 mismatches
!
! 1 AGGCATACATGACN{ }TCCATAGTAGTAGTAGTACATATACGACAGACTCAGTGAAGGCCGATTCAQ
```

> 0 <
01/10 Intelligenetics
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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "36_38_40iss" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "SPECTOR091n.key":

36_38_40 (NA) ID 36_38_40 NA preliminary pattern
1 followed by
2 acccataacatgaac
2 any number of any character
2 tccattagtagtagtactatcactacgacactcagtgaaagggccgattcaccatcttc
2 any number of any character
2 gatcgcgaggatccggtatgagcgtc

Selected data banks and files:

Data bank : Issued_NA , all entries

-- Output Parameters --

Format Options:

| | Format Options: | File Options: |
|-----------------------------|-----------------|----------------------|
| Nucleic acid code matching | Exact | Indirect file |
| Find non-matching hits only | No | Sequence or key file |
| Report key used | Yes | List of hits |
| Note position of hit | Yes | Hit display |
| Display full annotations | Yes | Name and annotations |
| Sequence context | 50 | |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | NO |

No hits found.

-- Search Statistics --

| Times: | CPU | Total Elapsed |
|--------------------------------|-------------|---------------|
| | 00:06:48.06 | 00:16:47.00 |
| Number of sequences searched: | | 325093 |
| Number of sequence hits: | | 0 |
| Number of separate matches: | | 0 |
| Number of sequence hits saved: | | 0 |

```
!SEQUENCE LIST 1.0
! FINDPATTERNS on geneseqn:* allowing 0 mismatches
!      1 AGGCATAACATGACN[1]CCATAGTAGTAGTAGTAGTACATATACTACGCAGACTCAGTGAAAGGCCGATTTCAC
```

!!SEQUENCE_LIST 1.0
! FINDPATTERNS on EST: * allowing 0 mismatches
!
1 AGCCATACATGAACN()TCCATTAGTAGTAGTAGTACATATACCTACGACAGACTGAGTGAAGGGCCGATTCAC

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Quest - Quick User-directed Expression Search Tool
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-- Outline of search "37_39_41" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "Spector091p.key":

Selected sequence key from "37_39_41 AA preliminary pattern

37_39_41 (AA) ID 37_39_41 AA preliminary pattern

Followed by

1 shmm

2 any number of any character

2 issssyiyadvskgrffls

2 any number of any character

2 drgstgmdv

Selected files:

File : 37_39_4lags.pep

-- Output Parameters --

Format options:

| Format options: | File Options: |
|-----------------------------|---------------|
| Nucleic acid code matching | Exact |
| Find non-matching hits only | No |
| Report key used | Yes |
| Note position of hit | Yes |
| Display full annotations | Yes |
| Sequence context | 50 |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | NO |

1 match found in sequence:

aa06717 : Antibody 12B5 single chain Fv (scfv) fragment.

(from "37_39_4lags.pep")

TotG of: aa06717 Check: 1357 from: 1 to: 279

ID AAY06717 standard; Protein; 245 AA.

XX AAY06717;

XX

DT 17-JUN-1999 (first entry)

DE Antibody 12B5 single chain Fv (scfv) fragment.

XX

KM Agonist antibody; thrombopoietin receptor; TPO-R; thrombopoietin; DIC;

KM megakaryocyte; platelet; immunological; hematopoietic; thrombocytopenia;

KM bone marrow hypoplasia; disseminated intravascular coagulation; anemia;

KM myelodysplasia; myelotoxic chemotherapy; leukemia; tumour; Musk; CDR;

KM neuromuscular; muscular dystrophy; complementarity determining region.

KW

XX

OS Homo sapiens.

XX

XX

FT Key Location/Qualifiers

FT Misc-difference 208

FT /note= "unspecified"

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PR 25-AUG-1997; 97US-0918148.

XX (GETH) GENENTECH INC.

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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "37_39_4liss" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence. "sequence key from "spectro09lp.key":

1 37_39_41 (AA) ID 37_39_41 AA preliminary pattern
followed by
2 shmm
2 any number of any character
2 issssyiyadsvkygrftis
2 any number of any character
2 drgstlgndv

Selected data banks and files:

Data bank : Issued_AA , all entries

-- Output Parameters --

Format Options:

| | File Options: | |
|-----------------------------|---------------|-----|
| Nucleic acid code matching | Exact | NO |
| Find non-matching hits only | No | NO |
| Report key used | Yes | Yes |
| Note position of hit | Yes | Yes |
| Display full annotations | Yes | Yes |
| Sequence context | 50 | Yes |

-- Run Parameters --

| Run mode | Batch |
|--------------------------|-------|
| Time to start comparison | now |
| Notify at end of run | No |

No hits found.

-- Search Statistics --

| Times: | CPU | Total Elapsed |
|--------------------------------|-------------|---------------|
| | 00:02:03.08 | 00:06:38.00 |
| Number of sequences searched: | | 197390 |
| Number of sequence hits: | | 0 |
| Number of separate matches: | | 0 |
| Number of sequence hits saved: | | 0 |

!!SEQUENCE_LIST 1.0
! FINDPATTERNS on Swiss-Prot: * allowing 0 mismatches
! 1 SHNMNX{ } ISSSSYIYADSVKGRFTISX{ } DRGSTGMDV

Septem

!!SEQUENCE_LIST 1.0
! FINDPATTERNS on sptreml:* allowing 0 mismatches
! 1 SHNMNX()ISSSSXYIYADSVKGRFTISX()DRGSTGMDV

Septen
